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REFERENCE	1 (bases 1 to 2740)		
AUTHORS	Kim,I.G., Jun,D.Y., Sohn,U. and Kim,Y.H.		
TITLE	Kloning and expression of human mitotic centromere-associated kinesin gene		
JOURNAL	Biochim. Biophys. Acta 1359 (3), 181-186 (1997)		
MEDLINE	98094213		
REFERENCE	2 (bases 1 to 2740)		
AUTHORS	Kim,I.G., Jun,D.Y. and Kim,Y.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-JUL-1996) Microbiology, Kyungpook National University, Taegu 702-701, Korea		
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 Kim,H.J., Yi,J.Y., Sung,H.S., Moore,D.D., Jhun,B.B., Lee,Y.C. and  
 Lee,J.W.  
 TITLE Activating signal cointegrator 1, a novel transcription coactivator  
 of nuclear receptors, and its cytosolic localization under  
 conditions of serum deprivation  
 JOURNAL Mol. Cell. Biol. 19 (9), 6323-6332 (1999)  
 MEDLINE 99384300  
 PUBMED 10454579  
 REFERENCE 2 (bases 1 to 2160)  
 AUTHORS Kim,H.J., Moore,D.D. and Lee,J.W.  
 TITLE Direct Submission  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2002, 06:02:13 / Search time 47164.5 Seconds  
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Title: PCT-US02-13994-9

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Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
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18: em\_in:\*  
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33: em\_hlg\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	1668.8	94.8	2521	9	AF307851	AF307851 Homo sapi
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6	1474.2	83.8	2184	9	MACP53A	L20442 Rhesus monk
7	1401	79.6	1317	6	AR101808	AR101808 Sequence
8	1313.8	74.6	1317	6	A67149	A67149 Sequence
9	1313.8	74.6	1317	6	AR123180	AR123180 Sequence
10	1313.8	74.6	1317	6	AR157699	AR157699 Sequence
11	1313.8	74.6	1317	6	AX057140	AX057140 Sequence
12	1313.8	74.6	1317	6	AX203243	AX203243 Sequence
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15	1310.6	74.5	1317	6	128707	128707 Sequence
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28	1177.8	66.9	1181	6	AR080323	AR080323 Sequence
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36	1177.2	66.9	1484	6	BD000772	AR052767 Sequence
37	1177.2	66.9	1512	6	AR052767	AR052763 Sequence
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39	1175.6	66.8	1483	6	AR127894	AR127894 Sequence
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43	1174.2	66.7	1179	9	HSP53007	X60018 Human mRNA
44	1172.6	66.6	1179	9	HSP53002	X60011 Human mRNA
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## ALIGNMENTS

RESULT 1  
LOCUS HUMPS3T 1760 bp mRNA linear PRI 07-JAN-1995  
DEFINITION Human p53 cellular tumor antigen mRNA, complete cds.  
ACCESSION K03199  
VERSION K03199.1 GI:189478  
KEYWORDS antigen; antigen p53.  
SOURCE Human vulva carcinoma (cell line M31), CDNA to mRNA, clone pR4-2.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1760)  
AUTHORS Harlow, E.  
JOURNAL Unpublished (1985)  
REFERENCE 2 (bases 1 to 1760)  
AUTHORS Harlow, E., Williamson, N.W., Rajston, R., Helfman, D.M. and Adams, T.E.  
TITLE Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53  
JOURNAL Mol. Cell. Biol. 5 (7), 1601-1610 (1985)  
MEDLINE 85267676  
REFERENCE 3 (sites)  
AUTHORS McBride, O.W., Merry, D. and Givol, D.  
TITLE The gene for human p53 cellular tumor antigen is located on

chromosome 17 short arm (17p13)  
Proc. Natl. Acad. Sci. U.S.A. 83 (1), 130-134 (1986)  
86094327  
[3] sites: chromosomal location,  
draft entry and sequence for (2). [1] were kindly submitted via  
electronic mail by E. Harlow 17-OCT-1985. [1] reports that  
positions 1-79 may be a cloning artifact generated by ligating  
second, unrelated cDNA to the 5' end of the p53 cDNA.  
location/Qualifiers

## FEATURES

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ORIGIN	1 bp upstream of Salt site; Chromosome 17p13 [unpublished (1985)]				

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Best Local Similarity	99.9%	Pred. No. 0			
Matches 1759; Conservative	0	Mismatches	1	Indels	0; Gaps 0

[illegible]

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2002, 06:14:36 ; Search time 47164.5 Seconds  
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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31: em\_htg\_inv :  
32: em\_htg\_other :  
33: em\_htgo\_inv :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

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 MEDLINE: 97299869  
 FEATURES: Location/Qualifiers

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CDS

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genCore version 4.5  
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OM nucleic - nucleic search, using SW model

Run on: July 27, 2002, 05:34:43 ; Search time 3956.53 Seconds

1251.930 Million cell updates/sec

Title:	PCT-US02-13994-3
Perfect score:	2885

Sequence: 1 ggaattcctctgtcgaaagt.....aaacaaagaagttaaaaattt 2885

Scoring table: IDENTITY\_NUC

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	0%
Maximum Match	10%	

Maximum Match 100%  
Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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3	2181.6	75.6	2233	22	AAAC89558	Human histone deac
4	1558.4	54.0	2601	22	AAK94456	Human full-length
5	953.6	33.1	8459	22	AAAC89557	Human histone deac
6	671	23.3	4189	21	AACT7054	Human ORF7609
7	669.6	23.2	4245	22	AAK59024	Human polyucleotid
8	668	23.2	1725	21	AAAS1856	Caspase 8-Interact
9	667	23.1	3208	22	AAH14008	Human cDNA sequenc

C	45	C	44	C	43	C	42	C	41	C	40	C	39	C	38	C	37	C	36	C	35	C	34	C	33	C	32	C	31	C	30	C	29	C	28	C	27	C	26	C	25	C	24	C	23	C	22	C	21	C	20	C	19	C	18	C	17	C	16	C	15	C	14	C	13	C	12	C	11	C	10																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
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## ALIGNMENTS

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KW	Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; prostate cancer; ss.
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OS	Homo sapiens.
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PN	WO9904265-A2.
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PD	28-JAN-1999.
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PF	15-JUL-1998; 98MO-US14679.
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PR	22-JUN-1998; 98US-0102322.
PR	17-JUL-1997; 97US-0896164.
PR	10-OCT-1997; 97US-0061599.
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PR	10-OCT-1997; 97US-0948705.
PR	11-OCT-1997; 97GB-0021697.
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QY	1081	ccctcgaaagaaacaaagaaagaaagctgtgacagaaacaaacagagagctctgtcgctggagagagagc	1141
Db	1081	ccctcgaaagaaacaaagaaagaaagctgtgacagaaacaaacagagagctctgtcgctggagagagagc	1141
QY	1141	ccctgaaacaaatgcccccggaagagctctccaaacgaagagtgaaagaaacaaagaaacatctgaagaa	1201
Db	1141	ccctgaaacaaatgcccccggaagagctctccaaacgaagagtgaaagaaacaaagaaacatctgaagaa	1201
QY	1201	ggagaaacgaagaaagaaatgagagaaagaaagaaagagaaatctgcaatccaaagctgttaagaaagca	1261
Db	1201	ggagaaacgaagaaagaaatgagagaaagaaagaaagagaaatctgcaatccaaagctgttaagaaagca	1261
QY	1261	ggagagaaagagtggtgtgtctgaaagaaagagccccaatctgaagaaacatctgctgtgaataaaagaa	1321
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QY	1321	aaatctctccaaagaaagcccaacgcgtgcgaacatcttgcaaggtgtacaaacaaagccctccaaagt	1381
Db	1321	aaatctctccaaagaaagcccaacgcgtgcgaacatcttgcaaggtgtacaaacaaagccctccaaagt	1381
QY	1381	ggccaaatctgtgccccaacaaagccctgtggacgttacaacaaatccctccatctgtgcacccctggggg	1441
Db	1381	ggccaaatctgtgccccaacaaagccctgtggacgttacaacaaatccctccatctgtgcacccctggggg	1441
QY	1441	caatgaagaaaccccacaaagaaacaccccgtaaaagaaacccctcttcaacaaagatgtgtgtctcaaga	1501
Db	1441	caatgaagaaaccccacaaagaaacaccccgtaaaagaaacccctcttcaacaaagatgtgtgtctcaaga	1501
QY	1501	caagcttcaatgactaaagaaacaaatgtacatgtgtgcagaaacaaacaaatgcaacccctgaagaaatgc	1561
Db	1501	caagcttcaatgactaaagaaacaaatgtacatgtgtgcagaaacaaacaaatgcaacccctgaagaaatgc	1561
QY	1561	tgagccgaagacaaagaaacatctgttcacccgctgcgaagagaaagagccctgtctgaacaaagtgcga	1621
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QY	1621	ggcgagatccgaagatcgcaaaagaaacaaatgtacaaatgaaatccaaagaaatgcaatctgtgaataacaa	1681
Db	1621	ggcgagatccgaagatcgcaaaagaaacaaatgtacaaatgaaatccaaagaaatgcaatctgtgaataacaa	1681
QY	1681	caaccgcgtctatggagacaaagctccctccaaacccgagaaagatgaaacagaaagaaagtgtct	17401



Result	No.	Score	Query Match	Length	DB	ID	Description
	1	2559	99.6	2569	20	AAK40071	Colon cancer assoc
	2	1077.8	42.0	2265	23	AA887446	DNA encoding novel
	3	63.4	2.5	1534	21	AAA70107	Plasmodium falci
	4	53.4	2.1	2750	14	AAQ38808	G6PD encoding sequen
	5	50.6	2.0	9789	17	AAT41852	cDNA encoding plas
	6	50	1.9	3501	21	AAAT0202	Plasmodium falci
	7	49.6	1.9	6292	22	AA56735	Tumour suppressor
c	8	49	1.9	2091	22	AA47015	Plasmodium falci
	9	48.8	1.9	1452	21	AA470123	Plasmodium falci

C 10	48.6	1.9	2930	22	AA81670	cDNA sequence enco
C 11	47.4	1.8	468	22	AA38555	Human fetal liver
C 12	47.4	1.8	468	22	AAK06674	Human brain expres
C 13	47.4	1.8	468	22	AAK32370	Human bone marrow
C 14	47.4	1.8	468	22	AAJ18216	Probe t6902 used t
C 15	47.4	1.8	5527	21	AAAW0212	Plasmodium falcipa
C 16	47	1.8	5527	21	ABL33316	Human immune syste
C 17	46.8	1.8	5252	24	ABL33134	Human immune syste
C 18	46.8	1.8	7442	24	AA546686	Tumour suppressor
C 19	46.2	1.8	17131	24	ABL33053	Human immune syste
C 20	45.8	1.8	8245	22	AA546448	Tumour suppressor
C 21	45.4	1.8	2314	18	AAAT84152	DNA encoding a Sta
C 22	45.4	1.8	12237	24	ABL34356	Human immune syste
C 23	45.2	1.8	6109	24	ABL32326	Human immune syste
C 24	45.2	1.8	6109	24	AA561077	Human gene regulat
C 25	45.2	1.8	7438	21	AAAV0106	Plasmodium falcipa
C 26	45	1.8	2844	24	ABL34347	Human immune syste
C 27	45	1.8	4250	22	AAK52408	Human polynucleoti
C 28	45	1.8	4590	7	AAAN60472	Sequence encoding
C 29	44.8	1.7	7351	24	ABL32028	Human immune syste
C 30	44.8	1.7	7938	23	AA539523	DNA encoding novel
C 31	44.8	1.7	9223	23	AA576397	DNA encoding novel
C 32	44.6	1.7	7620	21	AAAV0132	Plasmodium falcipa
C 33	44.4	1.7	4012	18	AAAV74358	Staphylococcus aur
C 34	44.4	1.7	6398	24	ABL33101	Human immune syste
C 35	44.4	1.7	12705	24	ABL32149	Human immune syste
C 36	44.4	1.7	1082138	21	AAK22305	Arabidopsis thalian
C 37	44.2	1.7	2760	20	AAK60137	DNA encoding the M
C 38	44.2	1.7	7634	24	ABL34131	Human immune syste
C 39	44.2	1.7	9905	24	ABL32062	Human immune syste
C 40	44	1.7	5940	21	AAAV0105	Plasmodium falcipa
C 41	43.8	1.7	910715	20	AAAX20248	Borrelia burgdorfe
C 42	43.8	1.7	16173	24	ABL34468	Human metastasis a
C 43	43.6	1.7	3399	17	AAAT05968	Chicken leucocytos
C 44	43.6	1.7	5454	21	AAAT0236	Plasmodium falcipa
C 45	43.6	1.7	7334	24	ABL34124	Human immune syste

## ALIGNMENTS

	RESULT	1	
XX	AAx40071		
ID	AAx40071 standard; DNA; 2569 bp.		
XX			
AC	AAx40071:		
XX			
DT	02-JUL-1999 (first entry)		
XX			
DE	Colon cancer associated gene.		
XX			
KW	Cancer associated antigen; diagnosis; research; treatment		
KW	breast cancer; colon cancer; gastric cancer; renal can		
KW	prostate cancer; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	MO9904265-A2.		
XX			
PD			
XX	28-JAN-1999.		
PF			
XX	15-JUL-1998; 98WO-US14679.		
PR			
PR	23-JUN-1998; 98US-0102322.		
PR	17-JUL-1997; 97US-0896184.		
PR	10-OCT-1997; 97US-0061599.		
PR	10-OCT-1997; 97US-0061765.		
PR	10-OCT-1997; 97US-0948705.		
PR	11-OCT-1997; 97GB-0021697.		
XX			
PA	(LUDW-) LUDWIG INST CANCER RES.		
PI	Chen Y, Gout I, Gure A, O'Hare M, Odata Y, Old LJ		

PI pfreundschuh M, Sahlin U, Scanlan MJ, Stockert E;  
PI Tureci O;

DR WPI: 1999-132448/11.

XX New isolated cancer associated nucleic acids and polypeptides -  
PT Isolated using sera from cancer patients, used to develop products  
PT for the diagnosis, monitoring or treatment of cancers

PS Claim 67: Page 677-678: 787pp: English.

XX The invention relates to a method for diagnosing a disorder characterised  
CC by expression of a human cancer associated antigen precursor coded for by  
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a  
CC biological sample isolated from a subject with an agent that specifically  
CC binds to the NAM, an expression product or a fragment of an expression  
CC product complexed with an HLA molecule; and (b) determining the  
CC interaction between the agent and the NAM or the expression product as a  
CC determination of the disorder. The products and methods can be used in  
CC the diagnosis, monitoring, research, or treatment of conditions  
CC characterised by the expression of various cancer associated antigens.  
CC The invention provides nucleic acid sequences and encoded polypeptides  
CC which are cancer associated antigen precursors expressed in human breast  
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and  
CC lung cancer.

XX Sequence 2569 BP: 865 A; 418 C; 564 G; 712 T; 10 other;

Query Match 99.6%; Score 2559; DB 20; Length 2569;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2569: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 aagaagaaagcactctcttcagagagaaatagagatcttcgtgacaaagattggc 60  
OY 61 tctgaaattctgtggtccacagaaagactataatgctcgtgatttaaaacactata 120  
DB 61 tctgaaattctgtggtccacagaaagactataatgctcgtgatttaaaacactata 120  
OY 121 tcttctcatataaagaccttcagactttatgtaactaataaagaataaactga 180  
DB 121 tcttctcatataaagaccttcagactttatgtaactaataaagaataaactga 180  
OY 121 tcttctcatataaagaccttcagactttatgtaactaataaagaataaactga 180  
DB 121 tcttctcatataaagaccttcagactttatgtaactaataaagaataaactga 180  
OY 181 aattagtcactcttcagagagataaacaagtgttaaaacaaagccgaataatctaga 240  
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DB 241 tccaccttcgaaagagagagataatgtagctgttcccaagaagataattatgta 300  
OY 301 tctgtctgatacagaagagcaaacacaaatgacctctctcgtgacagttatagatta 360  
DB 301 tctgtctgatacagaagagcaaacacaaatgacctctctcgtgacagttatagatta 360  
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DB 361 tggcaatgttctcgtgttataactacaagaatagtaggcttgcacctgttataatgcaat 420  
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DB 421 attgcggggtgtgacatcatgctcctcgtcagggatttgaagttcctgcgaataaaaa 480  
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DB 481 tttcraagaagaatgtagtatacttcccaagagacagcagaggttcgaataaagtga 540  
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DB 541 atttgttaaatctcaagaacagatggagattatcttctgtgatacaatgtagatcagc 600

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DB 721 tcttaactgtataatccagaaagaaatagtaagacttatgcactgtgataatg 780  
OY 781 accgagtaacttctgtgacagttctgtgatacaggaagaaactcagtttgaagaaga 840  
DB 781 accgagtaacttctgtgacagttctgtgatacaggaagaaactcagtttgaagaaga 840  
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DB 1141 aatgactattctcagataaataaacaagaagatggttgaataaatacactagaat 1200  
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DB 1381 gaatttaagtaataaagctgtacaaataaataatataatggaacacagacagatgagct 1440  
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DB 1441 tgcgtgaataaactgaaaaaagatgtaaacattatgtgaacaaacaaagtaactccgtga 1500  
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ID	AAS87446 standard; cDNA; 2265 BP

AC MAS87446;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #23250

**KM** Human; chromosome mapping; gene mapping; gene therapy; forensic;  
**KM** food supplement; medical imaging; diagnostic; genetic disorder; ss

X

X5	Homo sapiens.
PN	MO200175067-A2.
XX	11-OCT-2001.
PD	
XX	30-MAR-2001; 2001MO-D0508631.
PF	
XX	31-MAR-2000; 2000US-0540217.
PR	23-APR-2000; 2000US-0649167.
PA	(HYSE-) HYSEQ INC.
PI	Drmannac RT, Liu C, Tang YT;
PT	MP1: 2001-639362/73.
DR	P-PADB: ABC23259.
XX	
PS	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
XX	
XX	Claim 1: SEQ ID NO 23250; 103bp; English.
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and genome mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. MAS64197-MAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pcr_sequences.
XX	
SQ	Sequence 2265 BP; 784 A; 356 C; 491 G; 634 T; 0 other:
Query Match	42.0%; Score 1077.8; DB 23; Length 2265;
Best Local Similarity	78.5%; Pred. No. 5e-257;
Matches 1496; Conservative	0; Mismatches 15; Indels 394; Gaps 2
Y	558 acagatgggaagtattcttctgcatgatgaacaatggatcatacagaatgatgattaaaga 617
Db	737 acagatgggaagtattcttctgcatgatgaacaatggatcatacagaatgatgattaaaga 796
Y	618 ggtatgccttcagtgaaaataaccgaatgaacctttccaccagaactaataaagtgcga 677
Db	797 ggtatgccttcagtgaaaataaccgaatgaacctttccaccagaactaataaagtgcga 856
Y	678 gtccaagtcctgttaacaataatcagcaatgtgcaacttcaagtattttctaacygtataac 737
Db	857 gtccaagtcctgttaacaataatcagcaatgtgcaacttcaagtattttctaacygtataac 916
Y	738 cagaaaaaaatatgatalaagacttaagcaactgtatagataggactgtgtaacttttgt 797
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Y	798 gtcaagttgcctgatacaggaataactcagtggtttaagaagaagaagaaacagactgctggag 857
Db	977 gtcaagttgcctgatacaggaataactcagtggtttaagaagaagaagaagaaacagactgctggag 1036



GenCore version 4.5  
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OK nucleic - nucleic search, using sw model

Run on: July 27, 2002, 05:39:00 ; Search time 3956.53 Seconds  
(without alignments)  
471.698 Million cell updates/sec

Title: PCT-US02-13994-8

Perfect score: 1087

Sequence: 1 aagatgacgctagtaaat.....aataatgattatattcaca 1087

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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19: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT.\*  
20: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT.\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT.\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT.\*  
23: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1087	100.0	1087	AA440070	Colon cancer assoc
2	1085	99.8	1435	AAV59766	Human secreted pro
3	1085	99.8	1435	AAV59765	Human secreted pro
4	1083.8	99.7	1368	AA52863	Human prostate tum
5	1083.4	99.7	1368	AA52863	Human prostate tum
6	1080.8	99.4	1328	AA33533	Human DNA demethyl
7	990.4	91.1	1640	AAV59616	Human secreted pro
8	846.4	77.9	1804	AA61218	Human DNA demethyl
9	600	55.2	1233	AA44351	Human nucleotide s

10	600	55.2	1233	22	AA48220	Heart muscle cell
11	600	55.2	1233	22	AA49586	Human coding sequ
12	275.4	25.3	1589	20	AA65219	Human DNA demethyl
13	261	24.0	2198	22	AA41434	Human CDNA sequenc
14	261	24.0	2198	20	AA61221	Human CDNA demethyl
15	254	23.4	726	22	AA403407	Human CDNA clone (
16	254	23.4	726	22	AA415254	Human CDNA sequenc
17	199.4	18.3	487	22	AA415254	Human CDNA clone (
18	140.4	12.9	145	16	AA40291	Human gene aligatu
19	109	10.0	155	22	AA43802	Human gene aligatu
20	105.6	9.7	295	22	AA59087	Human cancer relat
21	71.8	6.6	842	22	ABL13861	Drosophila melanog
22	71.8	6.6	1115	23	ABL18437	Drosophila melanog
23	71.8	6.6	3733	23	ABL18437	Drosophila melanog
24	71.8	6.6	3742	23	ABL18436	Drosophila melanog
25	71.8	6.6	4078	23	ABL15148	Drosophila melanog
26	51	4.7	51	22	AA130969	Human SNP oligonuc
27	49.4	4.5	51	23	ABL00202	Human silent nonco
28	46.6	4.3	6564	24	ABL32123	Human immune syste
29	46	4.2	6131	24	ABL32880	Human immune syste
30	44.6	4.1	17721	24	ABL33729	Human immune syste
31	43.6	4.0	10189	24	ABL34160	Human immune syste
32	43.4	4.0	18624	24	ABL33702	Human immune syste
33	43.2	4.0	1563	24	ABL34352	Human immune syste
34	43.2	4.0	7696	22	AA546399	Human immune syste
35	43	4.0	14987	24	ABL32631	Tumour suppressor
36	42.2	3.9	5962	24	ABL33287	Human immune syste
37	42	3.9	6035	24	ABL33524	Human immune syste
38	42	3.9	9539	22	AA54547	Human immune syste
39	41.8	3.8	13606	22	AA54547	Chemically pretrea
40	41.8	3.8	13606	22	AA54547	Human immune syste
41	41.8	3.8	13606	24	ABL33810	Tumour suppressor
42	41.4	3.8	10647	24	AA561397	Human immune syste
43	41.2	3.8	7746	24	ABL33857	Human gene regulat
44	41.2	3.8	1057	18	AA74868	Human immune syste
45	41	3.8	5195	24	ABL33596	Staphylococcus aur

## ALIGNMENTS

RESULT 1	
ID	AA440070 standard; DNA: 1087 BP.
XX	AA440070:
XX	02-JUL-1999 (first entry)
XX	Colon cancer associated gene.
XX	Cancer associated antigen; diagnosis; research; treatment; human;
XX	breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
XX	prostate cancer; ss.
OS	Homo sapiens.
XX	WO9904265-A2.
PN	28-JAN-1999.
XX	15-JUL-1998; 98MO-US14679.
XX	22-JUN-1998; 98US-0102322.
PR	17-JUL-1997; 97US-0896164.
PR	10-OCT-1997; 97US-0061599.
PR	10-OCT-1997; 97US-0061765.
PR	10-OCT-1997; 97US-0948705.
PR	11-OCT-1997; 97GB-0021697.
XX	(LUDW-) LUDWIG INST CANCER RES.
PA	Chen Y, Gout I, Gure A, O'Hare M, Ohta Y, Old LJ;
XX	
PI	

PI Pfreundschuh M, Sahlin U, Scanlan MJ, Stockert E;  
PI Tureci O;

DR WPI: 1999-132448/11.

PT New isolated cancer associated nucleic acids and polypeptides -  
PT Isolated using sera from cancer patients, used to develop products  
PT for the diagnosis, monitoring or treatment of cancers

PS Claim 67; Page 676-677; 787pp; English.

CC The invention relates to a method for diagnosing a disorder characterized  
CC by expression of a human cancer associated antigen precursor coded for by  
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a  
CC biological sample isolated from a subject with an agent that specifically  
CC binds to the NAM, an expression product or a fragment of an expression  
CC product complexed with an HLA molecule; and (b) determining the  
CC interaction between the agent and the NAM or the expression product as a  
CC determination of the disorder. The products and methods can be used in  
CC the diagnosis, monitoring, research, or treatment of conditions  
CC characterized by the expression of various cancer associated antigens.  
CC The invention provides nucleic acid sequences and encoded polypeptides  
CC which are cancer associated antigen precursors expressed in human breast  
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and  
CC lung cancer.

CC Sequence 1087 BP; 386 A; 212 C; 203 G; 286 T; 0 other;

Query Match 100.0%; Score 1087; DB 20; Length 1087;  
Best Local Similarity 100.0%; Pred. No. 1.2e-265;

Matches 1087; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aagatgagcctgaataatcacagaaagacagagacgtcgaaagacgtcctcaat 60  
DB 1 aagatgagcctgaataatcacagaaagacagagacgtcgaaagacgtcctcaat 60  
OY 61 caaataagggtaaacccagcttgatatacattgccaattagacaacagctcaat 120  
DB 61 caaataagggtaaacccagcttgatatacattgccaattagacaacagctcaat 120  
OY 121 ttcaaacacacccgtaaaccaagtcacaaatccatccatagtaataagtaacagacca 180  
DB 121 ttcaaacacacccgtaaaccaagtcacaaatccatccatagtaataagtaacagacca 180  
OY 121 ttcaaacacacccgtaaaccaagtcacaaatccatccatagtaataagtaacagacca 180  
DB 121 ttcaaacacacccgtaaaccaagtcacaaatccatccatagtaataagtaacagacca 180  
OY 181 caaagaatgataagacagcagcttcctctggggaagagagctcaagagctagt 240  
DB 181 caaagaatgataagacagcagcttcctctggggaagagagctcaagagctagt 240  
OY 181 caaagaatgataagacagcagcttcctctggggaagagagctcaagagctagt 240  
DB 181 caaagaatgataagacagcagcttcctctggggaagagagctcaagagctagt 240  
OY 241 gcatcagatgtaaacagacaatattataaaacacatggaactcccaagagctccaagga 300  
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DB 301 gttggtccagatgaatgatgagaccctttatctgctgtgttcagagtgcttgacaca 360  
OY 301 gttggtccagatgaatgatgagaccctttatctgctgtgttcagagtgcttgacaca 360  
DB 301 gttggtccagatgaatgatgagaccctttatctgctgtgttcagagtgcttgacaca 360  
OY 361 agctctgagccaatcacagagcagagctcgcgtcgtgtggaagaagacccgtcgtttg 420  
DB 361 agctctgagccaatcacagagcagagctcgcgtcgtgtggaagaagacccgtcgtttg 420  
OY 421 cttaacacatctcaaccctctgcaaaagcttttatgtcacagatgagacatcaggaaa 480  
DB 421 cttaacacatctcaaccctctgcaaaagcttttatgtcacagatgagacatcaggaaa 480  
OY 481 caggagaagagcagatcacagcagaagcagaagaaattggaagaagcagcagatc 540  
DB 481 caggagaagagcagatcacagcagaagcagaagaaattggaagaagcagcagatc 540  
OY 541 ttgtcgagagctgctgatacagaagaagatgataatgaaatggaacagtgagatgaagcc 600  
DB 541 ttgtcgagagctgctgatacagaagaagatgataatgaaatggaacagtgagatgaagcc 600

OY 601 taagaatatgacagtaacttgcagccagcttccccaagagaaaattcctagaattg 660  
DB 601 taagaatatgacagtaacttgcagccagcttccccaagagaaaattcctagaattg 660  
OY 661 aacaaaatgcttcacagctgcttgcctgtgaagaaaaaatgtaaccagacataaga 720  
DB 661 aacaaaatgcttcacagctgcttgcctgtgaagaaaaaatgtaaccagacataaga 720  
OY 721 gcttttaataagcactaaccaatgcttttagatgataatgataatgataatgata 780  
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OY 781 ttcaaaaatctggttt 840  
DB 781 ttcaaaaatctggttt 840  
OY 841 gcagagccctaaagatgaagctgagctttgtgacagagtcacaaattactgaaatgac 900  
DB 841 gcagagccctaaagatgaagctgagctttgtgacagagtcacaaattactgaaatgac 900  
OY 901 acttaagtaaacattgtttcccccaggttttaataagaagacagatcagaattctaa 960  
DB 901 acttaagtaaacattgtttcccccaggttttaataagaagacagatcagaattctaa 960  
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DB 961 taatttccagttaaagattatgtgacttccactcactgataataacattattactt 1020  
OY 1021 atggaaggggagacacgtgacattcttcacatgcgcaactgttaagaacaaataatgatt 1080  
DB 1021 atggaaggggagacacgtgacattcttcacatgcgcaactgttaagaacaaataatgatt 1080  
OY 1081 attcaaca 1087  
DB 1081 attcaaca 1087

RESULT 2  
AAV59766 standard; DNA; 1455 BP.  
ID AAV59766;  
XX  
AC AAV59766;  
XX  
DT 19-JAN-1999 (first entry)  
XX  
DE Human secreted protein gene 106 clone HT3AM65.  
XX  
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
OS Homo sapiens.  
XX  
PN M09839448-A2.  
XX  
PD 11-SEP-1998.  
XX  
PF 06-MAR-1998; 98MO-US04493.  
XX  
PR 02-OCT-1997; 97US-0061060.  
PR 07-MAR-1997; 97US-0038621.  
PR 07-MAR-1997; 97US-0040161.  
PR 07-MAR-1997; 97US-0040162.  
PR 07-MAR-1997; 97US-0040163.  
PR 07-MAR-1997; 97US-0040333.  
PR 07-MAR-1997; 97US-0040334.  
PR 07-MAR-1997; 97US-0040336.  
PR 07-MAR-1997; 97US-0040626.

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2002, 05:40:04 ; Search time 3956.53 Seconds

(Without alignments)  
847.494 Million cell updates/sec

Title: PCT-US02-13994-10

Sequence: 1953

Sequence: 1 accgctgcagagagcagcc.....aaagaatgtttgacattt 1953

Scoring table:

IDENTITY\_MTC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDSI/gcgdata/hold-geneeq/geneeqn-emb1/NA2001A.DAT.\*  
23: /SIDSI/gcgdata/hold-geneeq/geneeqn-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgdata/hold-geneeq/geneeqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1953	100.0	1953	20 AAX39673
2	1953	100.0	1953	22 AAH02880
3	1791.2	91.7	1953	22 AAH02880
4	1253.2	64.2	22	AAH02893
5	577.6	29.6	22	AAH02893
6	577.6	29.6	22	AAH02893
7	544.8	27.9	22	AAH02893
8	482.4	24.7	20	AAH02893
9	482.4	24.7	21	AAH02893

10	482.4	24.7	549	23	AAH02893	Human lung tumour-
11	478	24.5	25423	22	AAH02893	Human digestive sy
12	478	24.5	25423	22	AAH02893	Human colorectal c
13	478	24.5	25424	22	AAH02893	Human digestive sy
14	478	24.5	25424	22	AAH02893	Human colorectal c
15	404.8	20.7	416	22	AAH02893	Human lung tumour
16	359	18.4	424	20	AAH02893	Human lung tumour
17	359	18.4	424	20	AAH02893	Human lung tumour
18	359	18.4	424	20	AAH02893	Human lung tumour
19	316.6	16.2	2923	23	AAH02893	Human lung tumour
20	313.2	16.0	726	20	AAH02893	Human lung tumour
21	305.4	15.6	6568	24	AAH02893	Human lung tumour
22	287.4	14.7	338	16	AAH02893	Human lung tumour
23	279.6	14.3	6568	24	AAH02893	Human lung tumour
24	249	12.7	2506	23	AAH02893	Human lung tumour
25	227	11.6	575	22	AAH02893	Human lung tumour
26	227	11.6	575	22	AAH02893	Human lung tumour
27	227	11.6	575	22	AAH02893	Human lung tumour
28	227	11.6	575	22	AAH02893	Human lung tumour
29	227	11.6	575	22	AAH02893	Human lung tumour
30	227	11.6	575	22	AAH02893	Human lung tumour
31	224	11.5	238	22	AAH02893	Human lung tumour
32	224	11.5	238	22	AAH02893	Human lung tumour
33	224	11.5	238	22	AAH02893	Human lung tumour
34	224	11.5	238	22	AAH02893	Human lung tumour
35	224	11.5	238	22	AAH02893	Human lung tumour
36	224	11.5	238	22	AAH02893	Human lung tumour
37	145.6	7.5	212	16	AAH02893	Human lung tumour
38	137.6	7.0	5895	23	AAH02893	Human lung tumour
39	136.6	7.0	291	21	AAH02893	Human lung tumour
40	127	6.5	2156	20	AAH02893	Human lung tumour
41	123	6.3	3017	19	AAH02893	Human lung tumour
42	123	6.3	3107	22	AAH02893	Human lung tumour
43	123	6.3	6483	22	AAH02893	Human lung tumour
44	120.6	6.2	2431	22	AAH02893	Human lung tumour
45	118.8	6.1	511	21	AAH02893	Human lung tumour

#### ALIGNMENTS

RESULT 1	AAH02893	standard; DNA; 1953 BP.
ID	AAH02893	
AC	AAH02893	
XX	AAH02893	
XX	AAH02893	
DT	02-JUL-1999	(first entry)
DE	Renal Cancer associated gene.	
XX		
XX	Cancer associated antigen; diagnosis; research; treatment; human.	
XX	breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;	
XX	prostate cancer; ss.	
XX		
OS	Homo sapiens.	
XX		
XX	MO9904265-A2.	
XX		
XX	28-JAN-1999.	
XX		
XX	15-JUL-1998;	98MO-US14679.
XX		
PR	22-JUL-1998;	98US-0103322.
PR	17-JUL-1997;	97US-0896164.
PR	10-OCT-1997;	97US-0061599.
PR	10-OCT-1997;	97US-0061765.
PR	10-OCT-1997;	97US-0948705.
PR	11-OCT-1997;	97GB-0021697.
XX		
PA	(LUDW-) LUDWIG INST CANCER RES.	
XX		
XX	Chen Y, Gout I, Gure A, O'Hare M, Ohta Y, Old LJ;	





Human MAGC-1 gene. Homo	Human MAGC-1 gene. Homo
Tumour rejection a	Tumour rejection a
MAGE-1 nucleic acid	MAGE-1 nucleic acid
Probe #1933 for gene	Probe #1933 for gene
Probe #5031 for gene	Probe #5031 for gene
Probe #5139 used to	Probe #5139 used to
Tumour rejection a	Tumour rejection a
MAGE-3 gene. Homo	MAGE-3 gene. Homo
Tumour rejection a	Tumour rejection a
Human melanoma anti	Human melanoma anti
MAGE-3 cDNA. Homo	MAGE-3 cDNA. Homo
Antigen E gene. Homo	Antigen E gene. Homo
Tumour rejection a	Tumour rejection a
Antigen E coding s	Antigen E coding s
M2-10E1 antigenic DN	M2-10E1 antigenic DN
MAGE-51 genomic DN	MAGE-51 genomic DN
Tumour rejection a	Tumour rejection a
MAGE-51 gene. Homo	MAGE-51 gene. Homo
MAGE-51 gene. Homo	MAGE-51 gene. Homo
E antigen precursor a	E antigen precursor a
Tumour rejection a	Tumour rejection a
MAGE-41 gene. Homo	MAGE-41 gene. Homo
Tumour rejection a	Tumour rejection a
MAGE-4 gene. Homo	MAGE-4 gene. Homo
MAGE-41 gene. Homo	MAGE-41 gene. Homo
MAGE-4 gene. Homo	MAGE-4 gene. Homo
MAGE-5 cDNA. Homo	MAGE-5 cDNA. Homo
Tumour rejection a	Tumour rejection a
MAGE-5 coding sequ	MAGE-5 coding sequ
MAGE-6 cDNA. Homo	MAGE-6 cDNA. Homo
Human MAGC-48 gene	Human MAGC-48 gene
cDNA encoding human	cDNA encoding human
Tumour rejection a	Tumour rejection a
Nucleotide sequenc	Nucleotide sequenc
Human MAGC-43 DNA	Human MAGC-43 DNA
MAGE-31 gene. Homo	MAGE-31 gene. Homo







QY 3961 aaataatctctctctcactgctgctgttcttctccttcaactcagcatctgctgtg 4202  
 Db 3961 aaataatctctctctcactgctgctgttcttctccttcaactcagcatctgctgtg 4202  
 QY 4021 ggaagcccttggttaagtagtggaatgaagtaagcagcagcagcagcagcagcagcagc 4080  
 Db 4021 ggaagcccttggttaagtagtggaatgaagtaagcagcagcagcagcagcagcagcagc 4080  
 QY 4081 gctgttagagcctagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 4140  
 Db 4081 gctgttagagcctagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 4140  
 QY 4141 agaggaatctgaag 4200  
 Db 4141 agaggaatctgaag 4200  
 QY 4201 gtgc 4204  
 Db 4201 gtgc 4204

## RESULT 2

AAA37927 ID AAA37927 standard: cDNA: 4204 BP.

AAA37927:

18-AUG-2000 (first entry)

Human MAGE-A3 nucleotide sequence.

MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine; cancer; human; tumor; tumor associated gene product; ss.

OS Homo sapiens.

PN M0200020581-A1.

13-APR-2000.

15-SEP-1999; 99MO-US21230.

05-OCT-1998; 98US-0166448.

(LDDM-) LUDWIG INST CANCER RES.

(UTVR-) UNIV VIRJIE BROUSEL.

Chaux P, Strobant V, Boon-Fallieur T, Van Der Bruggen P; Schultz ES, Van Snick J, Lethe B, Thielemans K, Corhals J; Heirman C;

WPI: 2000-317713/27.

P-PSDB: AAB02565.

New MAGE-A3 class II binding peptides, useful to diagnose and treat tumors, are fragments of MAGE-A3 which bind to and are presented to T lymphocytes by human leukocyte antigen class II molecules.

Example 6: Page 96-98; 119pp: English.

The present invention relates to MAGE-A3 (tumor associated gene product) human leukocyte antigen (HLA) class II-binding peptides (see AAB02565-802395, and AAB02633-802637). These peptides are presented to T cells in the context of HLA class II molecules. The peptides stimulate the activity and proliferation of CD4+ T lymphocytes. The invention also includes nucleotide sequences encoding MAGE-A3 peptides (see AAA37928 and AAA37938-A37940). The peptides and nucleotide sequences can be used to create antibodies against the MAGE-A3 peptides, the antibodies, peptides and nucleotide sequences can be used to create a vaccine. The peptides are used to diagnose or treat a disorder characterized by expression of MAGE-3, particularly cancer. The methods can also be used in the diagnosis of disorders associated with MAGE-3 expression. Included

CC In the invention are other human tumor antigen (see AAB02396-802637).  
 CC and PCR primers used in the course of the invention (see AAA37929-A37937  
 CC and AAA37941-A37942).  
 XX Sequence 4204 BP: 944 A; 1144 C; 1223 G; 893 T; 0 other;

Query Match 100.0%; Score 4204; DB 21; Length 4204;

Best Local Similarity 100.0%; Pred. No. 0; Matches 4204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acgcaagcagtagtctcaaccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 60  
 Db 1 acgcaagcagtagtctcaaccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 60  
 QY 61 tcagagtcag 120  
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 QY 121 gctcagc 180  
 Db 121 gctcagc 180  
 QY 181 cccaactcccccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240  
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 QY 301 aatccagttccacccctgc 360  
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 QY 361 tgacttcgcatgag 420  
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 QY 421 cctgaagtcgag 480  
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 QY 481 ggaag 540  
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 QY 541 tgcctgcgagcctgc 600  
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 QY 601 aacccgc 660  
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 QY 661 cagagcag 720  
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 QY 721 ccccgag 780  
 Db 721 ccccgag 780  
 QY 781 caaccac 840  
 Db 781 caaccac 840  
 QY 841 tccggcttggccctggtatcaagtcag 900  
 Db 841 tccggcttggccctggtatcaagtcag 900  
 QY 901 agtctcaggtacacatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 960  
 Db 901 agtctcaggtacacatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 960



Db 541 GATTACAGAGATCTGACCCAAAGGGGGAAACATGCTGACCCACAGACTGCTGA 600  
QY 601 ggaagaaagctggtgattcttgaagagatcaagacccctgaggaagatgaagtaact 660  
Db 601 GAGAAAGAGCTGCTGATTATGAAAGATCAGAGACCCCTGAGAGATGAGATTAAT 660  
QY 661 cccctcaagagatcagacacatgcccattgattgagagagaaagatggtgacttaagaa 720  
Db 661 CCCCTCAGGAGATACACACATGCCCAGATGAGAGAGAGAAAGCTGCTGACCTTCACGAA 720  
QY 721 catgggcatggtcgcgagccctcgtcatcaggtgacagagtg 766  
Db 721 CATGGGCAATGGCTGCGAGACCCCTGCTCATCAGGTGATAGCAAGTG 766  
RESULT 3  
LOCUS AR025465 931 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 2 from patent US 5798264.  
ACCESSION AR025465  
VERSION AR025465.1 GI:3978093  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 931)  
AUTHORS Pfreundschuh, M.  
TITLE Isolated nucleic acid molecules which encode renal cancer specific antigens, and uses thereof  
JOURNAL Patent: US 5798264-A 2 25-AUG-1998;  
FEATURES  
LOCATION/Qualifiers  
BASE COUNT 274 a 207 c 231 g 219 t  
ORIGIN  
Query Match 100.0%; Score 766; DB 6; Length 931;  
Best Local Similarity 100.0%; Pred. No. 1,2e-221;  
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 tggcccaaaaatgatggaagaagctggtccccccggggaagaaacaaactactctgaa 540  
Db 488 TGGCCCAAAAATGATAGGGAAGAGCTGTGCCCCGGGAAACCACTACCTCTGAGAA 547  
QY 541 gattcaagagatcctggaccaaaagggggagacatgctctgagaccacagactgctga 600  
Db 548 GATTCCAGAGATCTGAGCCAAAGGGGGAGAACTGCTGAGACCCACAGAGCTGCGA 607  
QY 601 ggaagaaagctggtgattcttgaagagatcagagcccttgaggagatgagtgact 660  
Db 608 GAGAAAGAGCTGCTGATTATGAAAGATCAGAGACCCCTGAGAGATGAGAGTAACT 667  
QY 661 cccctcaagagatcagacacatgcccattgattgagagagaaagatggtgacttaagaa 720  
Db 668 CCCCTCAGGAGATACACACATGCCCAGATGAGAGAGAGAAAGCTGCTGACCTTCACGAA 727  
QY 721 catgggcatggtcgcgagccctcgtcatcaggtgacagagtg 766  
Db 728 CATGGGCAATGGCTGCGAGACCCCTGCTCATCAGGTGATGCAAGTG 773  
RESULT 4  
LOCUS AR060380 931 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 2 from patent US 5840568.  
ACCESSION AR060380  
VERSION AR060380.1 GI:5986830  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 931)  
AUTHORS Pfreundschuh, M.  
TITLE Hodgkin's disease associated molecules and uses thereof  
JOURNAL Patent: US 5840568-A 2 24-NOV-1998;  
FEATURES  
LOCATION/Qualifiers  
BASE COUNT 274 a 207 c 231 g 219 t  
ORIGIN  
Query Match 100.0%; Score 766; DB 6; Length 931;  
Best Local Similarity 100.0%; Pred. No. 1,2e-221;  
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;